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RAW SEQUENCE LISTING  
PATENT APPLICATION: US/09/760,723

DATE: 06/08/2001  
TIME: 17:04:59

Input Set : A:\53466295.app  
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3 <110> APPLICANT: KOISHIHARA, YASUO  
 5 <120> TITLE OF INVENTION: INHIBITOR OF LYMPHOCYTE ACTIVATION  
 7 <130> FILE REFERENCE: 053466/0295  
 9 <140> CURRENT APPLICATION NUMBER: 09/760,723  
 C--> 10 <141> CURRENT FILING DATE: 2001-05-29  
 12 <150> PRIOR APPLICATION NUMBER: 09/367,833  
 13 <151> PRIOR FILING DATE: 1998-08-25  
 15 <150> PRIOR APPLICATION NUMBER: PCT/JP98/00831  
 16 <151> PRIOR FILING DATE: 1998-02-27  
 18 <160> NUMBER OF SEQ ID NOS: 8  
 20 <170> SOFTWARE: PatentIn Ver. 2.1  
 22 <210> SEQ ID NO: 1  
 23 <211> LENGTH: 1016  
 24 <212> TYPE: DNA  
 25 <213> ORGANISM: Homo sapiens  
 27 <220> FEATURE:  
 28 <221> NAME/KEY: CDS  
 29 <222> LOCATION: (23)..(562)  
 30 <223> OTHER INFORMATION: Nucleotide sequence of DNA coding for HM1.24  
 31 antigen  
 33 <400> SEQUENCE: 1  
 34 gaattcggca cgagggatct gg atg gca tct act tcg tat gac tat tgc aga 52  
 35 Met Ala Ser Thr Ser Tyr Asp Tyr Cys Arg  
 36 1 5 10  
 38 gtg ccc atg gaa gac ggg gat aag cgc tgt aag ctt ctg ctg ggg ata 100  
 39 Val Pro Met Glu Asp Gly Asp Lys Arg Cys Lys Leu Leu Leu Gly Ile  
 40 15 20 25  
 42 gga att ctg gtg ctc ctg atc atc gtg att ctg ggg gtg ccc ttg att 148  
 43 Gly Ile Leu Val Leu Ile Ile Val Ile Leu Gly Val Pro Leu Ile  
 44 30 35 40  
 46 atc ttc acc atc aag gcc aac agc gag gcc tgc cgg gac ggc ctt cgg 196  
 47 Ile Phe Thr Ile Lys Ala Asn Ser Glu Ala Cys Arg Asp Gly Leu Arg  
 48 45 50 55  
 50 gca gtg atg gag tgt cgc aat gtc acc cat ctc ctg caa caa gag ctg 244  
 51 Ala Val Met Glu Cys Arg Asn Val Thr His Leu Leu Gln Gln Glu Leu  
 52 60 65 70  
 54 acc gag gcc cag aag ggc ttt cag gat gtg gag gcc cag gcc acc 292  
 55 Thr Glu Ala Gln Lys Gly Phe Gln Asp Val Glu Ala Gln Ala Ala Thr  
 56 75 80 85 90  
 58 tgc aac cac act gtg atg gcc cta atg gct tcc ctg gat gca gag aag 340  
 59 Cys Asn His Thr Val Met Ala Leu Met Ala Ser Leu Asp Ala Glu Lys  
 60 95 100 105  
 62 gcc caa gga caa aag aaa gtg gag gag ctt gag gga gag atc act aca 388  
 63 Ala Gln Gly Gln Lys Lys Val Glu Glu Leu Glu Gly Glu Ile Thr Thr  
 64 110 115 120  
 66 tta aac cat aag ctt cag gac gcg tct gca gag gtg gag cga ctg aga 436  
 67 Leu Asn His Lys Leu Gln Asp Ala Ser Ala Glu Val Glu Arg Leu Arg

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68	125	130	135	
70	aga gaa aac cag gtc tta agc gtg aga atc gcg gac aag aag tac tac			484
71	Arg Glu Asn Gln Val Leu Ser Val Arg Ile Ala Asp Lys Lys Tyr Tyr			
72	140	145	150	
74	ccc agc tcc cag gac tcc agc tcc gct gcg gcg ccc cag ctg ctg att			532
75	Pro Ser Ser Gln Asp Ser Ser Ala Ala Pro Gln Leu Leu Ile			
76	155	160	165	170
78	gtg ctg ctg ggc ctc agc gct ctg ctg cag tgagatccca ggaagctggc			582
79	Val Leu Leu Gly Leu Ser Ala Leu Leu Gln			
80	175	180		
82	acatcttgaa aggtccgtcc tgctcggttt ttcgcttgaa cattcccttg atctcatcag			642
84	ttctgagcgg gtcatggggc aacacggta gcggggagag cacggggtag ccggagaagg			702
86	gcctctggag caggctctgaa gggccatgg ggcagtctg ggtgtggggcacacagtccgg			762
88	ttgaccagg gctgtctccc tccagagcct ccctccggac aatgagtccc ccctcttgc			822
90	tcccaccctg agattggca tgggtgcgg tgtggggggc atgtgctgcc tgggttatg			882
92	ggtttttttt gcgggggggg ttgctttttt ctgggtctt tgagctccaa aaaaataaaac			942
94	acttcctttt agggagagca ccacaccta aaaaaaaaaaaaaaaa aaaaaaaaaaaa			1002
96	ttcgggcggc cgcc			1016
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103	<213> ORGANISM: Artificial Sequence			
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106	<223> OTHER INFORMATION: Description of Artificial Sequence: DNA encoding L			
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108	antibody			
110	<220> FEATURE:			
111	<221> NAME/KEY: CDS			
112	<222> LOCATION: (1)..(378)			
114	<220> FEATURE:			
115	<221> NAME/KEY: sig_peptide/			
116	<222> LOCATION: (1)..(57)			
118	<220> FEATURE:			
119	<221> NAME/KEY: mat_peptide			
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125	-15	-10	-5	
127	gtc cac tcc gac atc cag atg acc cag agc cca agc agc ctg agc gcc			96
128	Val His Ser Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala			
129	-1 1	5	10	
131	agc gtg ggt gac aga gtg acc atc acc tgt aag gct agt cag gat gtg			144
132	Ser Val Gly Asp Arg Val Thr Ile Thr Cys Lys Ala Ser Gln Asp Val			
133	15	20	25	
135	aat act gct gta gcc tgg tac cag cag aag cca gga aag gct cca aag			192
136	Asn Thr Ala Val Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys			
137	30	35	40	45
139	ctg ctg atc tac tcg gca tcc aac cgg tac act ggt gtg cca agc aga			240

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140	Leu	Leu	Ile	Tyr	Ser	Ala	Ser	Asn	Arg	Tyr	Thr	Gly	Val	Pro	Ser	Arg
141				50				55						60		
143	ttc	agc	ggg	agc	ggg	agc	ggg	acc	gac	ttc	acc	ttc	acc	atc	agc	agc
144	Phe	Ser	Gly	Ser	Gly	Ser	Gly	Thr	Asp	Phe	Thr	Phe	Thr	Ile	Ser	Ser
145				65				70						75		
147	ctc	cag	cca	gag	gac	atc	gct	acc	tac	tac	tgc	cag	caa	cat	tat	agt
148	Leu	Gln	Pro	Glu	Asp	Ile	Ala	Thr	Tyr	Tyr	Cys	Gln	Gln	His	Tyr	Ser
149				80				85						90		
151	act	cca	ttc	acg	ttc	ggc	caa	ggg	acc	aag	gtg	gaa	atc	aaa	'c	
152	Thr	Pro	Phe	Thr	Phe	Gly	Gln	Gly	Thr	Lys	Val	Glu	Ile	Lys		
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158	<212>	TYPE:	DNA													
159	<213>	ORGANISM:	Artificial Sequence													
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163		chain V region	version r of humanized anti-HM1.24													
164		antibody														
166	<220>	FEATURE:														
167	<221>	NAME/KEY:	CDS													
168	<222>	LOCATION:	(1)..(417)													
170	<220>	FEATURE:														
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172	<222>	LOCATION:	(1)..(57)													
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175	<221>	NAME/KEY:	mat_peptide													
176	<222>	LOCATION:	(58)..(417)													
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180	Met	Asp	Trp	Thr	Trp	Arg	Val	Phe	Phe	Leu	Leu	Ala	Val	Ala	Pro	Gly
181								-15		-10					-5	
183	gct	cac	tcc	'cag	gtg	cag	ctg	gtg	cag	tct	ggg	gct	gag	gtg	aag	aag
184	Ala	His	Ser	Gln	Val	Gln	Leu	Val	Gln	Ser	Gly	Ala	Glu	Val	Lys	Lys
185					-1	1			5				10			
187	cct	ggg	gcc	tca	gtg	aag	gtt	tcc	tgc	aag	gca	tct	gga	tac	acc	ttc
188	Pro	Gly	Ala	Ser	Val	Lys	Val	Ser	Cys	Lys	Ala	Ser	Gly	Tyr	Thr	Phe
189														15	20	25
191	act	ccc	tac	tgg	atg	cag	tgg	gtg	cga	cag	gcc	cct	gga	caa	ggg	ctt
192	Thr	Pro	Tyr	Trp	Met	Gln	Trp	Val	Arg	Gln	Ala	Pro	Gly	Gln	Gly	Leu
193						30		35			40			45		
195	gag	tgg	atg	gga	tct	att	ttt	cct	gga	gat	ggg	gat	act	agg	tac	agt
196	Glu	Trp	Met	Gly	Ser	Ile	Phe	Pro	Gly	Asp	Gly	Asp	Thr	Arg	Tyr	Ser
197													50	55	60	
199	cag	aag	tcc	aag	ggc	aga	gtc	acc	atg	acc	gca	gac	aag	tcc	acg	agc
200	Gln	Lys	Phe	Lys	Gly	Arg	Val	Thr	Met	Thr	Ala	Asp	Lys	Ser	Thr	Ser
201													65	70	75	
203	aca	gcc	tac	atg	gag	ctg	agc	agc	ctg	aga	tct	gag	gac	acg	gcc	gtg
204	Thr	Ala	Tyr	Met	Glu	Leu	Ser	Ser	Leu	Arg	Ser	Glu	Asp	Thr	Ala	Val

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205	80	85	90	
207	tat tac tgt gcg aga gga tta cga cga ggg ggg tac tac ttt gac tac			384
208	Tyr Tyr Cys Ala Arg Gly Leu Arg Arg Gly Gly Tyr Tyr Phe Asp Tyr			
209	95	100	105	
211	tgg ggg caa ggg acc acg gtc acc gtc tcc tca'g			418
212	Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser			
213	110	115	120	
217	<210> SEQ ID NO: 4			
218	<211> LENGTH: 418			
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228	<222> LOCATION: (1)..(417)			
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234	<220> FEATURE:			
235	<221> NAME/KEY: mat_peptide			
236	<222> LOCATION: (58)..(417)			
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239	'atg gac tgg acc tgg agg gtc ttc ttc ctg gct gta gct cca ggt			48
240	Met Asp Trp Thr Trp Arg Val Phe Phe Leu Leu Ala Val Ala Pro Gly			
241	-15	-10	-5	
243	gct cac tcc cag gtg cag ctg gtg cag tct ggg gct gag gtg aag aag			96
244	Ala His Ser Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys			
245	-1 1	5	10	
247	cct ggg gcc tca gtg aag gtt tcc tgc aag gca tct gga tac acc ttc			144
248	Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe			
249	15	20	25	
251	act ccc tac tgg atg cag tgg gtg cga cag gcc cct gga caa ggg ctt			192
252	Thr Pro Tyr Trp Met Gln Trp Val Arg Gln Ala Pro Gly Gln Gly Leu			
253	30	35	40	45
255	gag tgg atg gga tct att ttt cct gga gat ggt gat act agg tac agt			240
256	Glu Trp Met Gly Ser Ile Phe Pro Gly Asp Gly Asp Thr Arg Tyr Ser			
257	50	55	60	
259	cag aag ttc aag ggc aga gtc acc atc acc gca gac aag tcc acg agc			288
260	Gln Lys Phe Lys Gly Arg Val Thr Ile Thr Ala Asp Lys Ser Thr Ser			
261	65	70	75	
263	aca gcc tac atg gag ctg agc agc ctg aga tct gag gac acg gcc gtg			336
264	Thr Ala Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val			
265	80	85	90	
267	tat tac tgt gcg aga gga tta cga cga ggg ggg tac tac ttt gac tac			384
268	Tyr Tyr Cys Ala Arg Gly Leu Arg Arg Gly Gly Tyr Tyr Phe Asp Tyr			
269	95	100	105	
271	tgg ggg caa ggg acc acg gtc acc gtc tcc tca'g			418

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272 Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser  
273 110 115 120  
276 <210> SEQ ID NO: 5  
277 <211> LENGTH: 180  
278 <212> TYPE: PRT  
279 <213> ORGANISM: Homo sapiens  
281 <220> FEATURE:  
282 <223> OTHER INFORMATION: Amino acid sequence of HM1.24 antigen  
284 <400> SEQUENCE: 5  
285 Met Ala Ser Thr Ser Tyr Asp Tyr Cys Arg Val Pro Met Glu Asp Gly  
286 1 5 10 15  
288 Asp Lys Arg Cys Lys Leu Leu Leu Gly Ile Gly Ile Leu Val Leu Leu  
289 20 25 30  
291 Ile Ile Val Ile Leu Gly Val Pro Leu Ile Ile Phe Thr Ile Lys Ala  
292 35 40 45  
294 Asn Ser Glu Ala Cys Arg Asp Gly Leu Arg Ala Val Met Glu Cys Arg  
295 50 55 60  
297 Asn Val Thr His Leu Leu Gln Gln Glu Leu Thr Glu Ala Gln Lys Gly  
298 65 70 75 80  
300 Phe Gln Asp Val Glu Ala Gln Ala Ala Thr Cys Asn His Thr Val Met  
301 85 90 95  
303 Ala Leu Met Ala Ser Leu Asp Ala Glu Lys Ala Gln Gly Gln Lys Lys  
304 100 105 110  
306 Val Glu Glu Leu Glu Gly Glu Ile Thr Thr Leu Asn His Lys Leu Gln  
307 115 120 125  
309 Asp Ala Ser Ala Glu Val Glu Arg Leu Arg Arg Glu Asn Gln Val Leu  
310 130 135 140  
312 Ser Val Arg Ile Ala Asp Lys Lys Tyr Tyr Pro Ser Ser Gln Asp Ser  
313 145 150 155 160  
315 Ser Ser Ala Ala Ala Pro Gln Leu Leu Ile Val Leu Leu Gly Leu Ser  
316 165 170 175  
318 Ala Leu Leu Gln  
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325 <213> ORGANISM: Artificial Sequence  
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328 <223> OTHER INFORMATION: Description of Artificial Sequence: Amino acid sequence  
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330 antibody  
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336 Val His Ser Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala  
337 -1 1 5 10  
339 Ser Val Gly Asp Arg Val Thr Ile Thr Cys Lys Ala Ser Gln Asp Val  
340 15 20 25  
342 Asn Thr Ala Val Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys

**VERIFICATION SUMMARY**

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Input Set : A:\53466295.app

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L:10 M:271 C: Current Filing Date differs, Replaced Current Filing Date